



Finishing and Investigating the Genomes of *Prochlorococcus*, *Synechococcus*, and *Nitrosomonas*: An Overview

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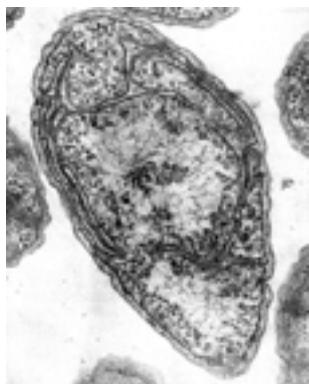
The ~~art~~ of Finishing at LLNL

- **Team:** 4 members
- **Goal:** charged with finishing 3 genomes (*Prochlorococcus marinus*, marine *Synechococcus*, *Nitrosomonas europaea*) in 6 months
- **Process:**
 - Evaluate genomes
 - Identify and sort out repeated elements (mask problematic ones)
 - Order and orient contigs
 - Primer design for walking (using shotgun clones) and PCR/walking
 - Alignments of contig ends
 - If available, alignment to similar genome
 - Multiplex PCR
 - Tackle repeat element structures

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Nitrosomonas europaea

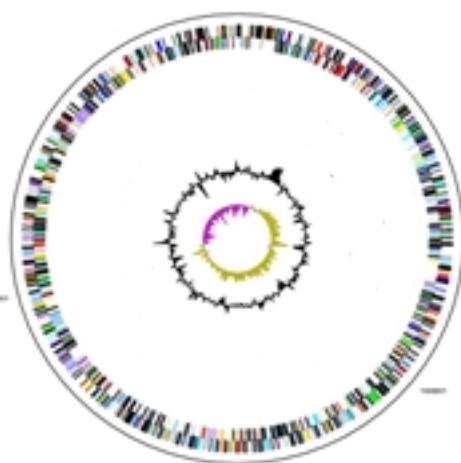


- Obligate chemolithoautotroph
- Requires inorganic compounds
- Uses ammonia as sole energy source
- Use CO₂ as carbon source
- β -proteobacteria
- Oxidizes ammonia to nitrite
- Best-studied nitrifier
 - Ammonia monooxygenase (2 x amoCAB)
 - Hydroxylamine oxidoreductase (3 x hao)
 - Tetraheme c cytochrome (3 x cycA)
- Soil, sewage, fresh water

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N. europaea sp. Schmidt (ATCC 25978) Genome



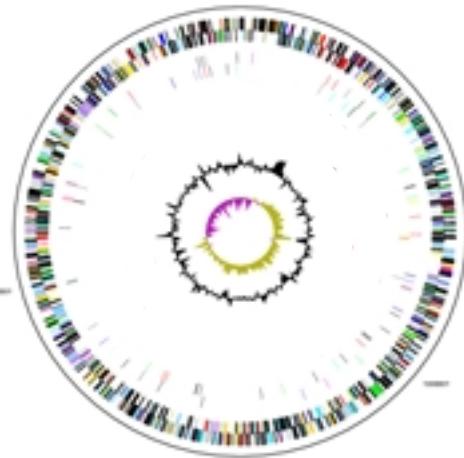
- 2 812 099 bp (50.7% G+C)
- 2604 predicted ORFs
- 89.1% coding
- 41 tRNAs
- One 16S-23S-5S rRNA operon
- 360 top hits to *Neisseria meningitidis*
- 451 to *Pseudomonas aeruginosa* (γ)

Many repeats (>5%)

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N. europaea sp. Schmidt (ATCC 25978) Genome

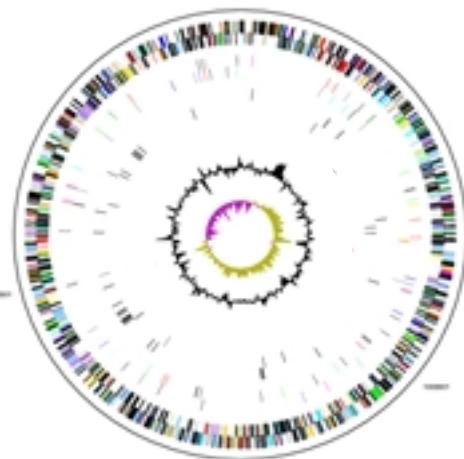


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- Many repeats (>5%)
- 8 families of IS elements (2-26 copies)

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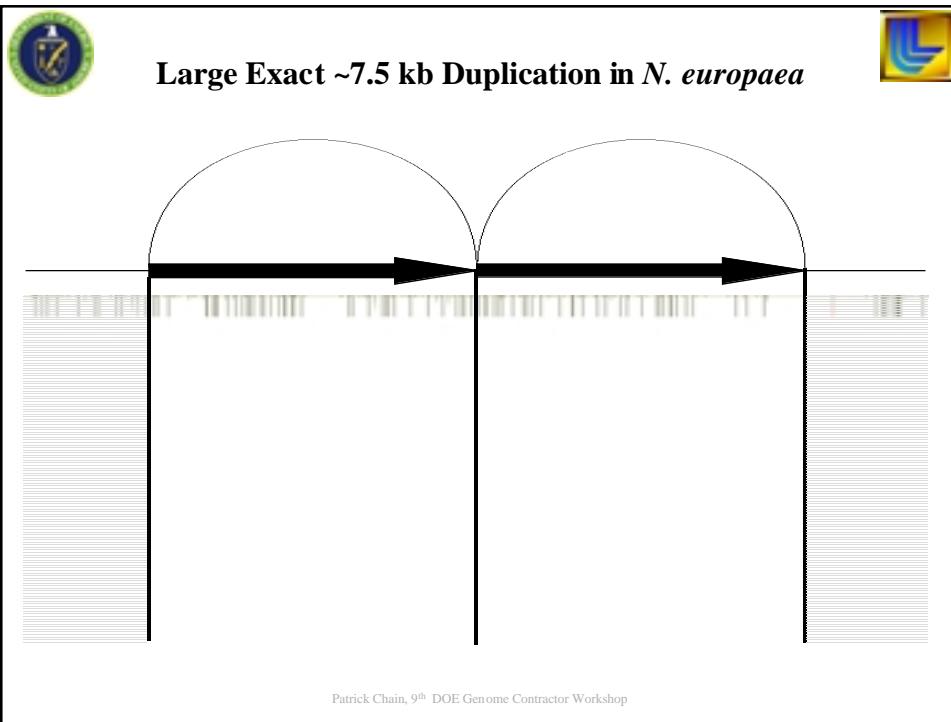
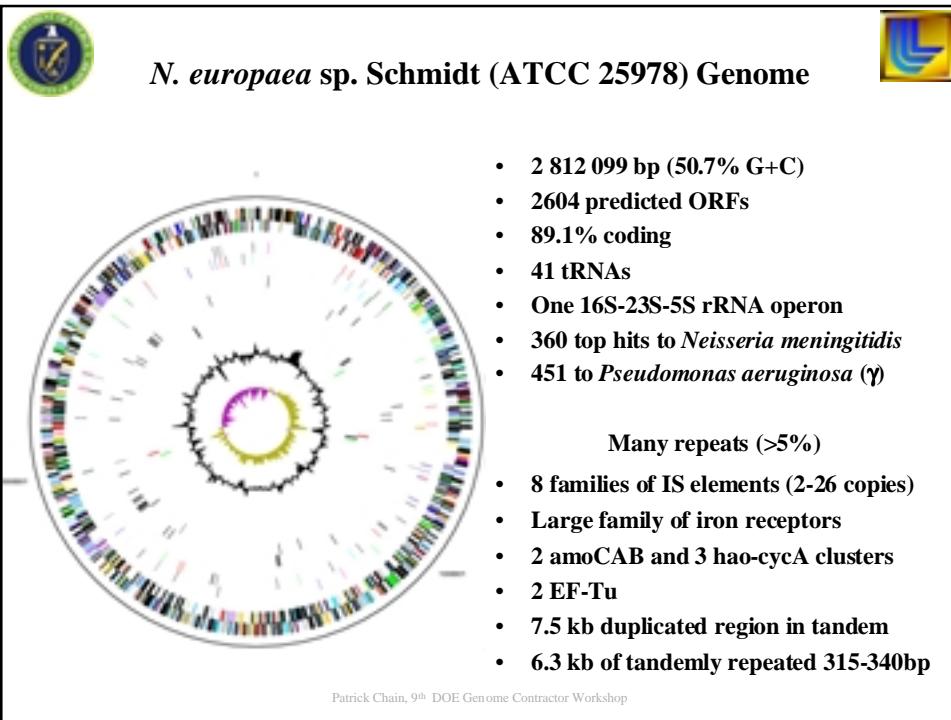


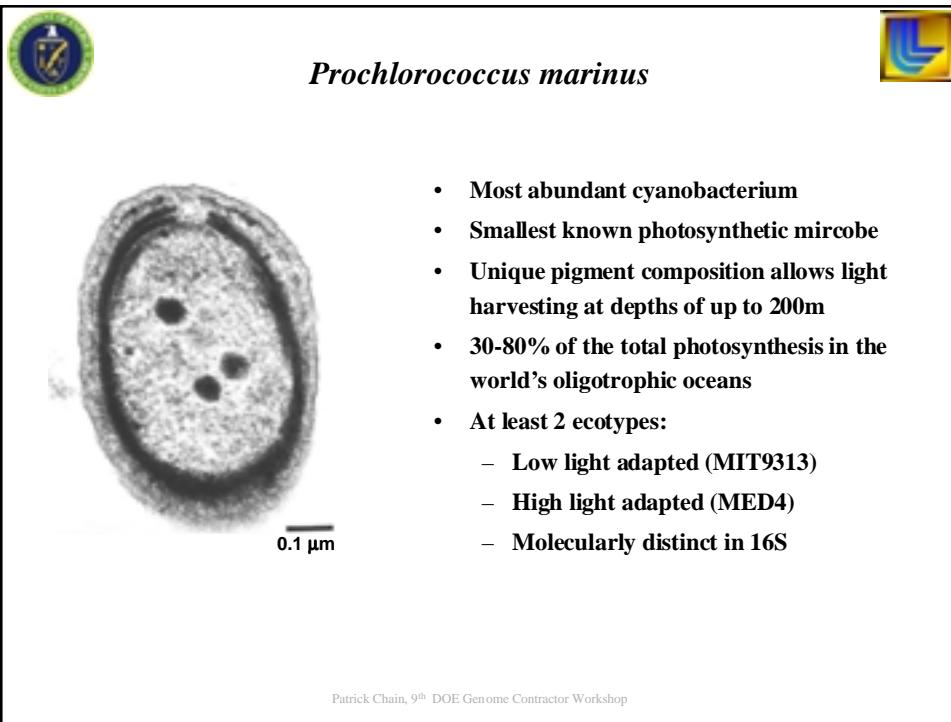
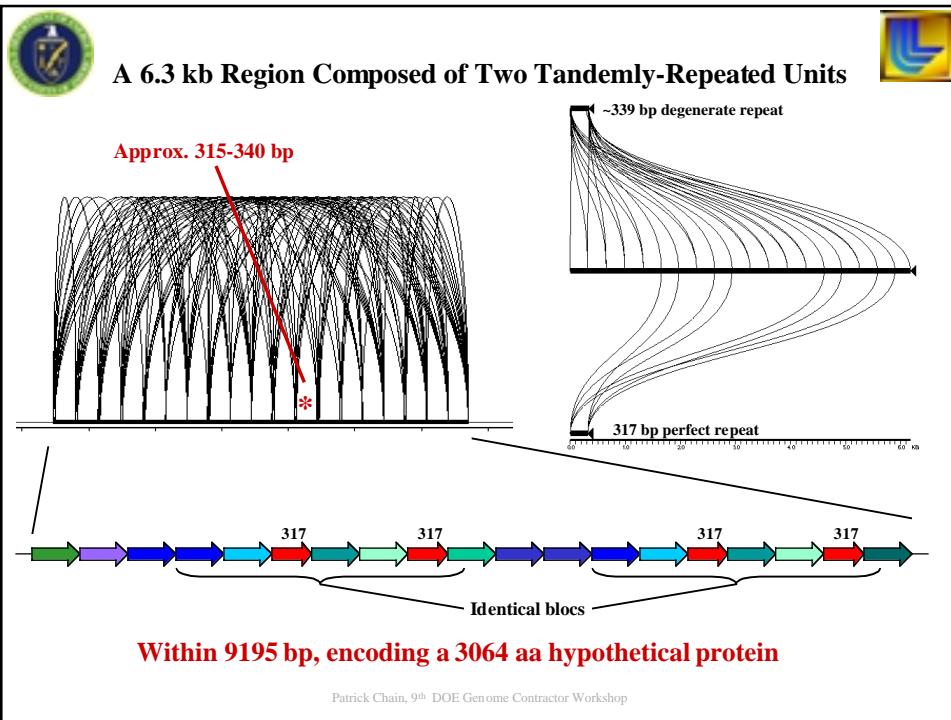
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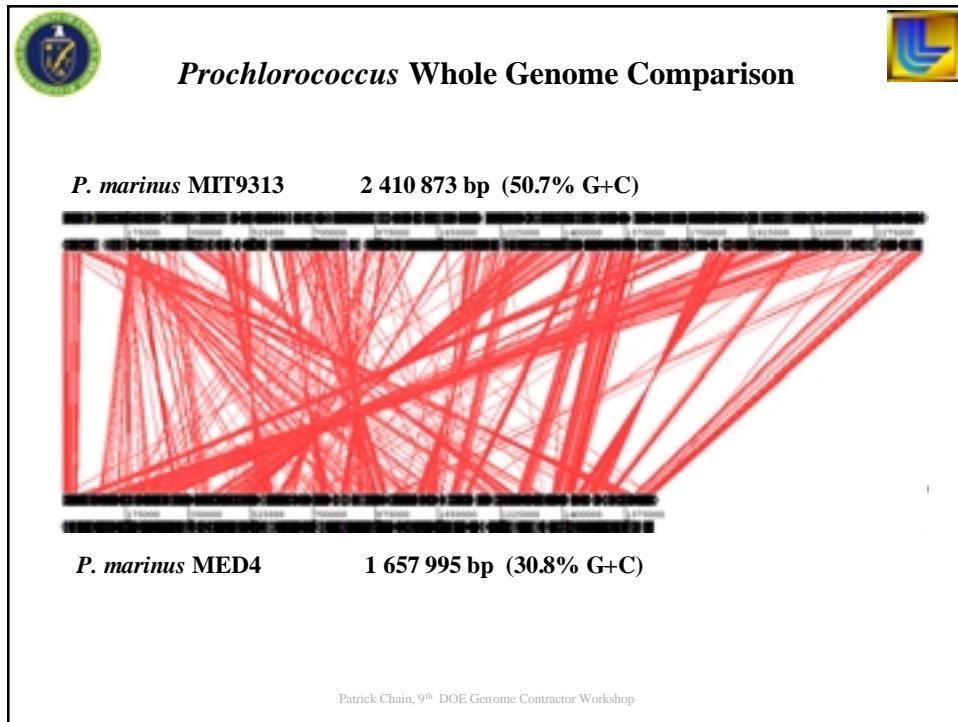
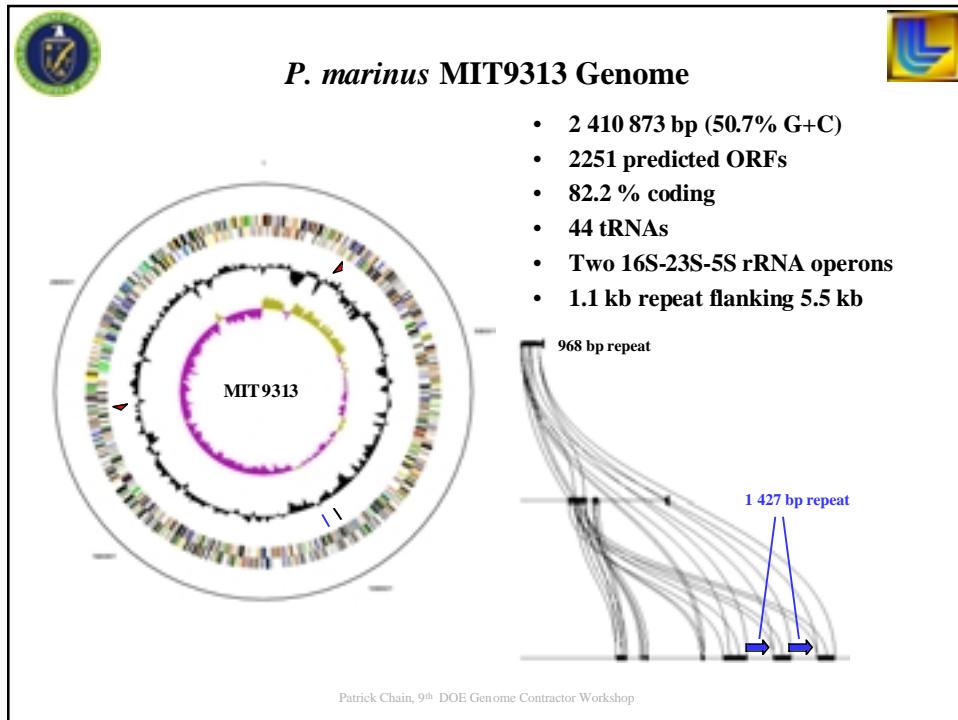


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- 8 families of IS elements (2-26 copies)
 - Large family of iron receptors

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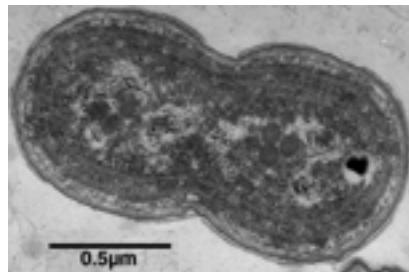








Marine *Synechococcus*

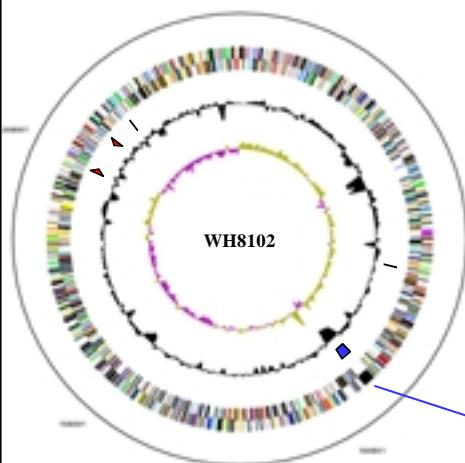


- Another abundant cyanobacterium
- 2 types of *Synechococcus*
 - Marine requires elevated $[Na^+Cl^-]$
- Coexists with and closely related to *Prochlorococcus*
- 1/3 of isolates possess a unique type of swimming motility (25 $\mu m/sec$)
 - No external organelle found
 - Respond to nitrogenous compounds
 - These isolates form a monophyletic cluster

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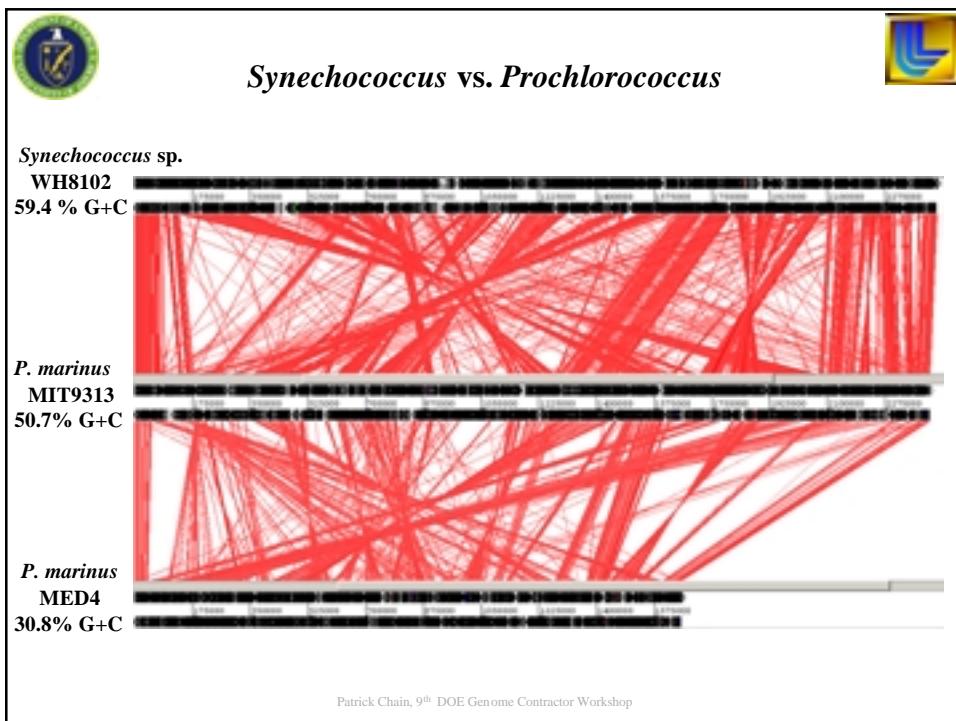
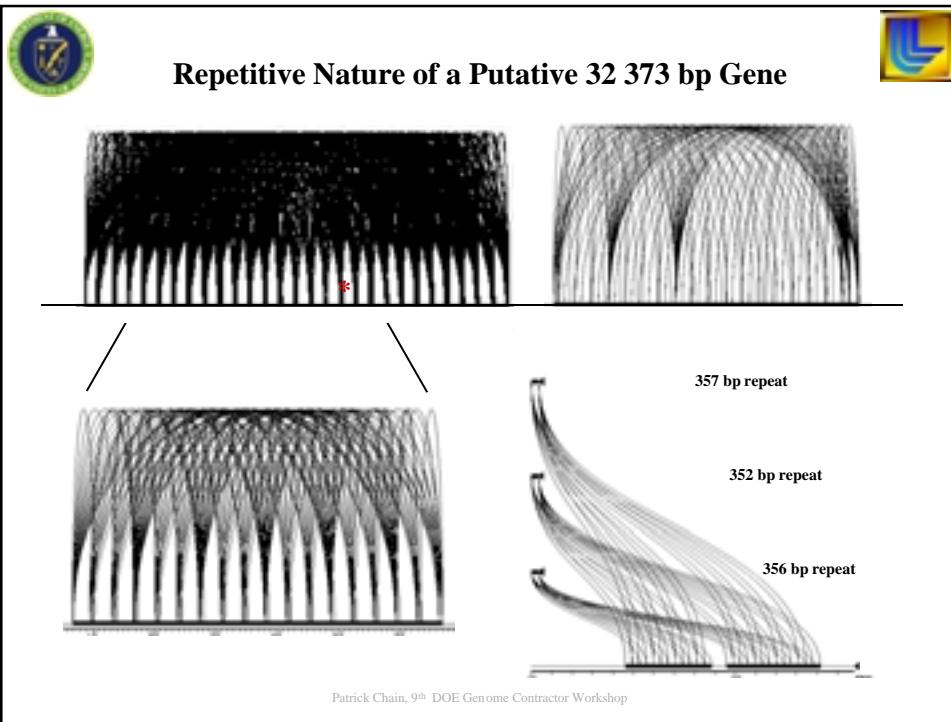


Synechococcus sp. WH8102 Genome



- 2 431 363 bp
 - 59.4 % G+C
 - 2523 predicted ORFs
 - 91.3 % coding
 - 42 tRNAs
- Repeats**
- Two 16S-23S-5S rRNA operons
 - 2 copies of photosystem II protein D
 - A complex region with 2 tandem repeats:
 - Highly degenerate repeat unit (7 kb total)
 - Relatively conserved repeat unit 28x (10 kb total)
 - Single ORF (>30 kb – 10 000 aa)

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Hofstadter's Law: "*It always takes longer than you expect, even when you take Hofstadter's Law into account.*"



Adapted from Drew Sheneman, The Newark Star Ledger

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